

03-10-614-934-14 (1-45) x AR359345 (1-138)

QY 1 MetMetIlePheCysGlnGlyGlnLySlysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
Db 1 ATGATGATTTCCTGCCAAGGCCAGAAATAATTATCGATGTAATAACGGTAG 60

QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysTyr 40
Db 61 TGTTATCCAGATTCATCAGATAATAACCAAGAGCAGCAGAATGTGTTATAAACCA 120

QY 41 CysBacnCysTyrPro 45
Db 121 TGCATATGTTACCA 135

RESULT 2

SYNCTX LOCUS SYNCTX Synthetic scorpion charybotoxin gene, 3' end. 151 bp DNA linear SYN 27-APR-1993
DEFINITION Synthetic scorpion charybotoxin gene, 3' end.
VERSION M64610
ACCESSION M64610_1 GI:208160
KEYWORDS charybotoxin; peptide blocker of K⁺ channels.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE Park,C.S., Hauberg,S.F. and Miller,C.
AUTHORS Design, synthesis, and functional expression of a gene for
TITLE charybotoxin, a peptide blocker of K⁺ channels
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (6), 2046-2050 (1991)
MEDLINE 9117749
PUBLMED 1706515
COMMENT Original source text: Synthetic DNA.
FEATURES source Location/Qualifiers

1. .151 /organism="synthetic construct"
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(db_xref="taxon:32630"
/gene="CTX"
<1..138
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>transl_table=11
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>protein_id="AAH73014_1"
>ob_xref="GI:208161"
>translation="VDGSIERGQFTNVSCSTSKECNWVCQRLHNTSRGKCMNKKRCY
S"
ORIGIN

Alignment Scores:
Pred. No.: 0.000188 Length: 151
Score: 102.00 Matches: 17
Percent Similarity: 58.97% Conservative: 6
Best Local Similarity: 43.59% Mismatches: 16
Query Match: 38.35% Indels: 0
DB: 12 GlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCys 25
Db 16 GAGAGTCGTCATTACCATGTTCTCTGACACTCTCAAGGAATGTTGTCGTTGT 75

QY 26 IleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
Db 76 CAACTCTGCTAACACACCGGGTAATGCTGAACAATAAATGTCGTTAC 132

RESULT 3

AR359343 LOCUS AR359343 Sequence 9 from patent US 6593141. 114 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 9 from patent US 6593141.
ACCESSION AR359343

VERSION AR359343..1 GI:33765590
KEYWORD SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 114)
AUTHORS Herman,R., Wong,J.F., Lu,A.L., Presnail,J.K. and Lee,J.-M.
TITLE Scorpion toxins
JOURNAL Patent: US 6593141-A 9 15-JUL-2003;
FEATURES source
1..114 /organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 0.00019 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: 6

US-10-614-934-14 (1-45) x AR359343 (1-114)

QY 12 AspTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThr 31
Db 10 AATGTGCCGTCAGAATGCTGCAACATGTCGTCAGTTGCATAAAAGAGTAATAAT 69

QY 32 ArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyrPro 45
Db 70 AATAGCGGAAAGTGCTATGACAATGTTATGTTATCCA 111

RESULT 4

AX063238 LOCUS AX063238 Sequence 3 from Patent WO0078958. 186 bp DNA linear PAT 24-JAN-2001
DEFINITION AX063238
VERSION AX063238..1 GI:12541063
KEYWORDS
ORGANISM Hottentotta judaica
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
REFERENCE 1 Buthidia; Buthoidea; Buthidiae; Hottentotta.
AUTHORS Herrmann,R., Lee,J.M. and Wong,J.F.
TITLE Scorpion toxins from buthotus judaicus
JOURNAL Patent: WO 0078958-A 3 28-DEC-2000;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
FEATURES source Location/Qualifiers
1. .186 /organism="Hottentotta judaica"
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(db_xref="taxon:6863";

ORIGIN

Alignment Scores:
Pred. No.: 0.00407 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: 6

US-10-614-934-14 (1-45) x AX063238 (1-186)

QY 1 MetMetIlePheCysGlnGlyGlnLySlysIleAsnTyrArgCysAsnSerGly 19
Db 46 ATGGTTATTCGAGCCACGCTCAAAGCAGTGTGAGTGAACGCTGATCGAGGAGAT 105

QY 20 GlucysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLys 39
Db 106 AATGCGGAAACCATGCTATGATAATAACGGCACAACTAAACTAAATGCTAACAT 165

QY 32 ArgAlaAlaLysCysIleAsnLysThrCysAsnCysTyr 44
 Db 259 TACAGGGGAAATGATGTAATGCGTTGTAT 297

RESULT 12
 AX063240 Locus AX063240 Definition Sequence 5 from Patent WO0078958. Accession AX063240 Version AX063240.1 GI:12541064
 Keywords SOURCE Hottentotta judaica
 ORGANISM Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Hottentotta.

REFERENCE 1 AUTHORS Herrmann, R., Lee, J.M. and Wong, J.F.
 TITLE Scorpion toxins from buthonus Judaicus
 JOURNAL Patent: WO 0078958-A 5 28-DEC-2000;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
 FEATURES Location/Qualifiers 1..180
 source /organism="Hottentotta judaica"
 /mol_type="unassigned DNA"
 /db_xref="taxon:6863"

ORIGIN

Alignment Scores:
 Pred. No.: 0.0177 Length: 180
 Score: 87.50 Matches: 18
 Percent Similarity: 46.67% Conservative: 3
 Best Local Similarity: 40.00% Mismatches: 23
 Query Match: 32.89% Indels: 1
 DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063240 (1-180)

QY 1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
 Db 46 ATGACCATATGTTAATGCCAAGTAGAACANATGTGAATGT--ACAGGTGGCTCA 102

QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaLysCysIleAsnLysThr 40
 Db 103 TGTGCTTCACATGAAAGAGTAAATTAGGAGTAGCTGCAGGAALATGCTTAATGGAGA 162

QY 41 CysAsnCysTyrPro 45
 Db 163 TGTGCTCTGCTATCCG 177

RESULT 13
 I18306 Locus I18306 Definition Sequence 2 from patent US 5494895. Accession I18306 Version I18306.1 GI:1598661
 Keywords SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 120) AUTHORS Garcia,M.L., Koo,G.C., Leonard,R.J., Lin,C.-C.S., Slaughter,R.S., Stevens,S.P. and Williamson,J.M.
 TITLE scorpion peptide margatoxin with immunosuppressant activity
 JOURNAL Patent: US 5494895-A 27-FEB-1996;
 FEATURES source 1..120 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN Alignment Scores:
 Pred. No.: 0.0157 Length: 120
 Score: 86.50 Matches: 15

QY 11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleArgIleTyrAsn 30
 Db 7 ATCACAGTTAAATGCACTCTCCGAAACAGTGCCTGCGCCGTCGAAGCTCAGTCGCT 66

QY 31 ThrArgAla--AlaLysCysIleAsnLysThrCysAsnCysTyrPro 45
 Db 67 CAGCTGCTGGCTAATGCTGACCGTAATGCAATGCTACCCG 114

RESULT 14
 AX063254 Locus AX063254 Definition Sequence 19 from Patent WO0078958. Accession AX063254 Version AX063254.1 GI:12541071
 Keywords SOURCE Hottentotta judaica
 ORGANISM Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Hottentotta.

REFERENCE 1 AUTHORS Herrmann, R., Lee, J.M. and Wong, J.F.
 TITLE Scorpion toxins from buthonus Judaicus
 JOURNAL Patent: WO 0078958-A 19 28-DEC-2000;
 E.I. DU PONT DE NEMOURS AND COMPANY (US)
 FEATURES Location/Qualifiers 1..174
 source /organism="Hottentotta judaica"
 /mol_type="unassigned DNA"
 /db_xref="taxon:6863"

ORIGIN

Alignment Scores:
 Pred. No.: 0.0231 Length: 174
 Score: 86.50 Matches: 17
 Percent Similarity: 52.27% Conservative: 6
 Best Local Similarity: 38.64% Mismatches: 20
 Query Match: 32.52% Indels: 1
 DB: 6 Gaps: 1

US-10-614-934-14 (1-45) x AX063254 (1-174)

QY 1 MetMetIlePheCysGlnGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGlu 20
 Db 40 ATATGATGTTCAACGAACTCAG--TTTATAGACGGAATTCACATCANCATAAGGA 96

QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaLysCysIleAsnLysThr 40
 Db 97 TGTGCTCTGCTATTGTAAGGAAAGATTGCTGCAGGAGACTGCTATAATGGAA 156

QY 41 CysAsnCysTyr 44
 Db 157 TGCCTTGTTAT 168

RESULT 15
 IAU427745 Locus IAU427745 Definition Androctonus australis txa gene for toxin Aatxi, exons 1-2. Accession AU427745 Version AU427745.1 GI:27652635
 Keywords SOURCE Androctonus australis (sahara scorpion)
 ORGANISM Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; Buthida; Buthoidea; Buthidae; Androctonus.

REFERENCE
 AUTHORS 1
 Vacher,H., Alami,M., Legros,C., Possani,L.D., Bougis,P.E. and
 Martin-Bauclaire,M.F.
 TITLE Novel toxins blocking A-type potassium currents: purification from
 venoms of diverse Androctonus species, amino acid sequence
 determination, pharmacological characterization and gene structure
 JOURNAL Unpublished
 REFERENCE 2
 AUTHORS (bases 1 to 263)
 Martin-Bauclaire,M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-JAN-2002) Martin-Bauclaire M.F., Universite de la
 Mediterranee, Institut Jean Roche UMR 6560 CNRS, Bd Pierre Dramard,
 F-133916 Marseille cedex 20, FRANCE
 FEATURES Location/Qualifiers
 SOURCE
 1. . 263
 /organism="Androctonus australis"
 /mol_type="genomic DNA"
 /db_xref="taxon:6058"
 /tissue_type="muscle"
 /country="Tunisia;Beni-Khedache"
 1. . 263
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 /db_xref="GI:27652036"
 /translation="MKFSSILILLLICMSMSIFNCQIETNKKQQGSSCASYVRRVIG
 VAAGKCKINGRCVCVP"
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 ORIGIN
 Alignment Scores:
 Pred. No.: 0.0354 Length: 263
 Score: 86.50 Matches: 18
 Percent Similarity: 48.84% Conservative: 3
 Best Local Similarity: 41.86% Mismatches: 21
 Query Match: 32.52% Indels: 1
 DB: 3 Gaps: 1
 US-10-614-934-14 (1-45) x AAU427745 (1-263)
 QY 3 IlePheCysGlnGlyGlnLysileAsnTyrArgCysSerAsnSerGlyGluCysIle 22
 Db 135 ATCTTCGGCAATTGCCAATTTGAAACAACTAGAAATGT---CANGGTGGATCGGTGCT 191
 QY 23 ProHisCysteIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCysAsn 42
 Db 192 TCAGATGTAGAGAGTAATTGGAGTAGCTCTGGCAAATGATATTATGGAGATGTGTC 251
 QY 43 CystTyrPro 45
 Db 252 TGCTAACCC 260

Search completed: August 19, 2005, 05:41:25
 Job time : 1765 secs

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GenCore version 5.1.6

MMIFCOCQKINRKNNSGE.....IRIYNTRAAKCINKTCNCYP 45

BLOSUM62

Xgapext 0.0 , Ygapext 0.5

Fgapext 6.0 , Fgapext 7.0

DelOp 6.0 , DelExt 7.0

Perfect score: 266

Sequence: 1 MMIFCOCQKINRKNNSGE.....IRIYNTRAAKCINKTCNCYP 45

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PR 22-JUN-1999; 99US-0140227P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Herrmann R, Lee J, Wong JF;
 XX WPI; 2001-071394/08.
 DR
 XX
 PT New polynucleotides encoding scorpion venom potassium-channel agonist controlling insect pest damage and parasitic worm infections.
 XX PS
 PT The present invention relates to scorpion toxins. The invention may be used for the creation of transgenic plants which express K-channel modifiers, useful as a means for controlling insect pests by producing insect-tolerant plants. In the prevention and/or treatment of insect pest damage and parasitic worm infections in animals and humans, the invention may also find use in creating specific new pesticides and antihelmintic drugs that are also non-toxic to humans, pets and livestock.
 CC Sequence 186 BP; 62 A; 31 C; 37 G; 56 T; 0 U; 0 Other;
 XX SQ
 Alignment Scores:
 Pred. No.: 0.00166 Length: 186
 Score: 92.50 Matches: 17
 Percent Similarity: 50.00% Conservative: 6
 Best Local Similarity: 34.96% Mismatches: 22
 Query Match: 34.77% Index: 1
 DB: 4 Gaps: 1
 US-10-614-934-14 (1-45) x AAF27524 (1-186)
 QY 1 MetMetIlePhcCysGlnGlyGlnLysLysIleAsnTyrargCys---AsnAsnSerGly 19
 Db 46 ATGGTTATTCGAGCCACGCCATACGACTGGGTGAATCGCTGTATGGAGGAGCAT 105
 QY 20 GluCysThrProCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLys 39
 Db 106 ATTGGGTAAACCATGCTATGATAAATACCGCACAATCAACTAAATGCTATGCTACGAT 165
 QY 40 ThrCysAsnCysTyrPro 45
 Db 166 CGGTGCAACTGTTATCCG 183
 RESULT 4
 AAQ4347 ID AAQ4347 standard; cDNA; 154 BP.
 AC XX
 XX AAQ4347;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-AUG-1995 (first entry)
 DE Synthetic gene for the expression of Margatoxin gene in E. coli.
 KW Scorpion venom; Centruroides margaritatus; margatoxin; Mgrtx;
 KW synthetic gene; oligo; ss.
 OS Synthetic.
 XX
 PN WO9503065-A1.
 XX
 PD 02-FEB-1995.
 XX
 PP 19-JUL-1994; 94WO-US008063.
 XX
 PR 22-JUL-1993; 93US-00096942.
 XX
 PA (MER) MERCK & CO INC.
 XX
 PI Garcia ML, Koo GC, Leonard RJ, Lin C, Slaughter RS, Stevens SP;

PI Williamson JM;
 XX
 DR WPI; 1995-075021/10.
 XX
 PT New purified scorpion venom peptide, Margatoxin - useful as a potent and selective inhibitor of a voltage-dependent potassium channel as an immunosuppressant.
 PT
 XX Claim 15; Page 22; 42PP; English.
 XX
 CC Margatoxin (MgTx) is purified to homogeneity from venom of the scorpion C. marginaritatus. The gene encoding MgTx is constructed and this gene is expressed in E. coli to produce recombinant MgTx. The MgTx gene was constructed using two synthetic oligos. The oligos are identical to AAQ84345 & AAQ84346 except for the 5' dcmP bases that were added to the 5' end of each to facilitate cutting with restriction enzymes. The two oligo sequences were combined to produce the gene having the coding strand on AAQ84347. Codon usage was optimised for high level expression in E. coli. It includes Sall Factor Xa, MgTx, and Hind III. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX SQ Sequence 154 BP; 41 A; 42 C; 37 G; 34 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.00178 Length: 154
 Score: 91.50 Matches: 16
 Percent Similarity: 58.50% Conservative: 8
 Best Local Similarity: 39.02% Mismatches: 16
 Query Match: 34.40% Index: 1
 DB: 2 Gaps: 1
 US-10-614-934-14 (1-45) x AAQ84347 (1-154)
 QY 6 GluGlyGlnLysLysIleAsnTyrargCysAsnAsnSerGlyGlucylsleProHisCys 25
 Db 16 GAAGGGTGATCCATCACATCACCTTAAATCGCTCTCGAAACAGTGCCGCCTGGC 75
 QY 26 IleArgIleTyrAsnThrArgAla--AlaLysCysIleAsnLysThrCysAsnCysTyr 44
 Db 76 AAAGCTCAGTTCGGTCAGTCGCTGGCTAAATGCTGAACGGTAATGCTAAATGCTAC 135
 QY 45 Pro 45
 DB 136 CCG 138
 RESULT 5
 AAF27525 ID AAF27525 standard; DNA; 180 BP.
 XX
 AC AAF27525;
 XX
 DT 28-MAR-2001 (first entry)
 DE Scorpion kalitoxin 2 precursor DNA #2.
 XX
 KW Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 XX
 OS Hotentotta judaica.
 XX
 PN WO200078958-A2.
 XX
 PD 28-DEC-2000.
 XX
 PP 21-JUN-2000; 2000WO-US017049.
 XX
 BR 22-JUN-1999; 99US-0140227P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Herrmann R, Lee J, Wong JF;
 XX
 DR WPI; 2001-071394/08.

PT New polynucleotides encoding scorpion venom potassium-channel agonist
 PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 PS Claim 1; Page 45; 50pp; English.

XX The present invention relates to scorpion toxins. The invention may be
 CC used for the creation of transgenic plants which express K-channel
 CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelminthic
 CC drugs that are also non-toxic to humans, pets and livestock.
 XX Sequence 180 BP; 59 A; 27 C; 36 G; 58 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 0.00742 Length: 180
 Score: 87.50 Matches: 18
 Percent Similarity: 46.67% Conservative: 3
 Best Local Similarity: 40.00% Mismatches: 23
 Query Match: 32.89% Indels: 1
 DB: 4 Gaps: 1
 US-10-614-934-14 (1-45) x AAF27525 (1-180)

QY 1 MetMetIleDpheCysGlnGlyGlnLysLysIleLeuLeuTyrArgCysAsnAsnSerGlyGlu 20
 Db 46 ATGACCATATGATTAATGCCAGTAGAAACAAATGTGAATG 102
 QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaLysCysIleAsnLysThr 40
 Db 103 TGTGCTCAACATGAAAGTAGTAAAGGAGTAGCTGCAAGAAATGCAATTATGGAAAGA 162
 QY 41 CysAsnCysTyrPro 45
 Db 163 TGTGCTGCTATTCGG 177

RESULT 6
 AAQ84344
 ID AAQ84344 standard; cDNA; 127 BP.
 XX
 AC AAQ84344;
 XX DT 25-MAR-2003 (revised)
 XX DT 24-AUG-1995 (first entry)
 XX DE Constructed gene encoding scorpion margatoxin (MgTX).
 XX KW Scorpion venom; Centruroides margaritatus; margatoxin; MgTX;
 XX KW synthetic gene; ss.
 OS Synthetic.
 XX FH Location/Qualifiers
 KEY 1: .117
 FT /tag= a
 PN WO9503065-A1.
 XX PD 02-FEB-1995.
 XX FT 19-JUL-1994; 94WO-US008063.
 XX PR 22-JUL-1993; 93US-00096942.
 XX PA (MERCK) MERCK & CO INC.
 XX PA Garcia MF, Koo GC, Leonard RJ, Lin C, Slaughter RS, Stevens SP;
 PI Williamson JM;
 XX DR WPI; 1995-07021/10.
 DR P-PSDB; AAR66876.

XX Sequence 127 BP; 35 A; 37 C; 28 G; 27 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 0.00648 Length: 127
 Score: 86.50 Matches: 15
 Percent Similarity: 58.33% Conservative: 6
 Best Local Similarity: 41.67% Mismatches: 14
 Query Match: 32.52% Indels: 1
 DB: 2 Gaps: 1
 US-10-614-934-14 (1-45) x AAQ84344 (1-127)

QY 11 IleAsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsn 30
 Db 7 ATCAACGTTAACGACCTCTCGAACAGTGCTGCCGCGCAAGCTCAGTCCGT 66
 QY 31 ThrArgAla--AlaLysCysIleAsnLysThrCysCysTyrPro 45
 Db 67 CAGTCGCTGGTGTAAATGCAAGACGTAATGCAAAATGCTACCG 114

RESULT 7
 AAF27532
 ID AAF27532 standard; DNA; 174 BP.
 XX
 AC AAF27532;
 XX DT 28-MAR-2001 (first entry)
 XX DE Scorpion Bmtx1 DNA.
 XX KW Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 XX OS Hottentotta judaica.
 XX PN WO200078958-A2.
 XX PD 28-DEC-2000.
 XX PF 21-JUN-2000; 2000WO-US017049.
 XX PR 22-JUN-1999; 99US-0140227P.
 XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Herrmann R, Lee J, Wong JF;
 XX DR WPI; 2001-071394/08.
 XX
 PT New polynucleotides encoding scorpion venom potassium-channel agonist
 PT proteins for production e.g. of insect-tolerant transgenic plants for
 PT controlling insect pest damage and parasitic worm infections.
 XX
 PS Claim 1; Page 48; 50pp; English.
 XX
 CC The present invention relates to scorpion toxins. The invention may be
 used for the creation of transgenic plants which express K-channel

CC modifiers, useful as a means for controlling insect pests by producing
 CC insect-tolerant plants. In the prevention and/or treatment of insect pest
 CC damage and parasitic worm infections in animals and humans, the invention
 CC may also find use in creating specific new pesticides and antihelmintic
 CC drugs that are also non-toxic to humans, pets and livestock
 XX SQ Sequence 174 BP; 51 A; 25 C; 37 G; 59 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 0.0096 Length: 174
 Score: 86.50 Matches: 17
 Percent Similarity: 52.27% Conservative: 6
 Best Local Similarity: 38.64% Mismatches: 20
 Query Match: 42.52% Indels: 1
 DB: 4 Gaps: 1
 US-10-614-934-14 (1-45) x AAF27532 (1-174)
 QY 1 MetMetAlaPheCysIleGlyGlnLysLysIleAlaSerTyrArgCysSerAlaSerGlyGlu 20
 Db 40 ATTAATGATTTCGACCGAAGCTCAG--TTTATAGACGTGAATGCACATCAGCTAGGAA 96
 QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 Db 97 TGTGGCCTATTGTTAGAAAGATTTGGTGGCCAGAGGAAAGTCATAATAAGCAA 156
 QY 41 CYSABnCYSTYR 44
 Db 157 TGCCGTTGTTAT 168
 RESULT 8
 ABQ97088
 ID ABQ97088 standard; cDNA; 231 BP.
 XX
 AC ABQ97088;
 XX DT 30-OCT-2002 (first entry)
 XX DE Mouse ES cell related cDNA SEQ ID NO 356.
 XX KW Mouse; ES cell; gene trapped sequence; GTS; gene expression; development disorder; cell differentiation disorder; gene; ss.
 XX OS Mus sp.
 XX PI US2002081668-A1.
 XX PD 27-JUN-2002.
 XX PP 30-NOV-2000; 2000US-00728446.
 XX PR 20-NOV-1998; 98US-0109302P.
 PR 01-DEC-1999; 99US-0168270P.
 XX PA (FRIE/) FRIEDRICH G.
 PA (ZAMB/) ZAMBROWICZ B.
 PA (SAND/) SANDS A T.
 PI Friedrich G, Zambrowicz B, Sands AT;
 XX DR WPI; 2002-626541/67.
 XX PT Novel murine polynucleotides that individually identify novel genes into
 PT which a retroviral gene trap vector has been integrated, useful in
 PT genomic analysis and in discovery, development of therapeutic and
 PT diagnostic agents.
 XX PS Claim 2; SEQ ID NO 356; 29pp + Sequence Listing; English.
 XX
 CC The invention relates to isolated murine polynucleotides (1) comprising a
 CC contiguous stretch of at least about 60 nucleotides of a sequence
 CC (ABQ973-AHQ8191) chosen from 1461 OMIM gene trapped sequences
 CC (GTRSA). The novel genes can be used in a process to identify novel

CC polynucleotide sequences by comparing them to the novel gene sequences.
 CC The novel genes and cells are useful in functional genomic analysis and
 CC in the discovery and development of new therapeutic and diagnostic agents
 CC and methods. (1) is useful for identifying the coding regions of the
 murine genome, to isolate cDNAs, genomic clones or full-length
 CC genes/polynucleotides or homologues, heterologues, paralogues or
 CC orthologues that are capable of hybridising to one or more of the GTS
 CC under stringent conditions. (1) can be incorporated into a phage display
 system that can be used to screen for proteins or other ligands, that are
 CC capable of binding an amino acid sequence encoded by an oligonucleotide
 CC or polynucleotide sequence in at least one of the GTS Sequences. (1) is
 CC useful in arrays, such as gene chips, to identify and characterise
 temporal and tissue specific gene expression, to identify the gene of
 interest from many sources and for genetic manipulations such as
 antisense inhibition and gene targeting. Decreasing the level of
 CC expression of (1) and/or down regulating the activity of peptides or
 CC proteins encoded by (1) is useful for treating development and cell
 CC differentiation disorders. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 sequidata.uspto.gov/sequence.html?docID=20020081668
 XX SQ Sequence 231 BP; 73 A; 47 C; 34 G; 77 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.119 Length: 231
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 6 Gaps: 1
 US-10-614-934-14 (1-45) x ABQ97088 (1-231)
 QY 4 PheCysGlyGlnLysLysIleAlaSerTyrArgCysSerAlaSerGlyGlu 20
 Db 84 TTTCCTCAGACAGAAAGCCCTCTCTTGAAATGAAATCATCAAATTTTGCGCT 143
 QY 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
 Db 144 TGTTCACATTGIGGGAGATAATCCCATCTCTATAATGCCACTAGTAAT 203
 QY 41 CYSABnCYSTYR 44
 Db 204 TGTAATGCTTT 215
 RESULT 9
 AAA8437
 ID AAA8437 standard; cDNA; 180 BP.
 XX
 AC AAA8437;
 XX DT 15-SEP-2000 (first entry)
 XX DE Scorpion potassium channel agonist Charybdotoxin 2 cDNA.
 XX KW Scorpion; charybdotoxin 2; potassium channel agonist; insecticidal;
 KW insect-tolerant transgenic plant; ss.
 XX OS Leurus quinquestratus.
 XX Key Location/Qualifiers
 FH FT CDS 1..180
 FT FT /*tag= "Charybdotoxin 2"
 FT FT /product= "Charybdotoxin 2"
 PN WO200032777-A2.
 XX PD 08-JUN-2000.
 XX PR 01-DEC-1999; 98WO-US028351.
 PR 02-DEC-1998; 98US-0110590P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PI Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
 XX DR WPI; 2000-422976/36.
 XX DR P-PSDB; AAY99580.
 XX PT New nucleic acid fragment encoding a scorpion toxin that is a potassium channel agonist, useful for creating transgenic plants that are more insect-tolerant.
 XX PS Claim 2; Page 42; 44pp; English.
 CC The present sequence encodes the scorpion potassium channel agonist Charybdotoxin 2. The toxin forms a compact structure kept rigid by three disulphide bonds. Potassium channels modulate a number of cellular events such as muscle contraction, neuro-endocrine secretion, frequency and duration of action potentials, electrolyte homeostasis and resting membrane potential. The agonist has a high affinity for the channel and may therefore act by producing an irreversible blockade of the channel. The nucleotide sequence was isolated from clone 1st-ph0018 e11 of a cDNA library representing mRNAs from Leirus scorpion telson tissues. The toxin is insecticidal and the cDNA sequence can therefore be used to create transgenic plants that express the toxin as a means of insect pest control. The amino acid sequence of the present toxin shows homology to the sequence of charybdotoxin 2 from Leirus quinquestriatus (AAY99588)
 XX Sequence 180 BP; 57 A; 29 C; 33 G; 61 T; 0 U; 0 Other;
 CC Alignment Scores:
 CC Pred. No.: 0.138
 CC Score: 78.00
 CC Percent Similarity: 56.67%
 CC Best Local Similarity: 43.33%
 CC Query Match: 29.32%
 CC DB:
 XX US-10-614-934-14 (1-45) x AAA48437 (1-180)
 QY 15 CYSAASnAsnSerGlyGluCysBileProHisCys1leArgileTyAsnThrArgAlaAla 34
 DB 85 TGCAGTCATCTGATCAATGGTGGTTGTCAAACTGTATAAACACTCATGCA 144
 QY 35 LYSCysIleAlaLysThrCysAsnCysTyr 44
 DB 145 AAGTGATGATAATAAATGCCGCTGTAT 174
 RESULT 10
 AAA48435
 ID AAA48435 standard; cDNA; 150 BP.
 AC AAA48435;
 DT 15-SEP-2000 (first entry)
 DE Scorpion potassium channel agonist Charybdotoxin cDNA.
 XX Scorpion; charybdotoxin; potassium channel agonist; insecticidal;
 KW insect-tolerant transgenic plant; ss.
 XX OS Leirurus quinquestriatus.
 XX Key Location/Qualifiers
 XX 1. . 150 CDS
 FT /*tag= a
 FT /partial= "Charybdotoxin"
 XX WO200032777-A2.
 XX PN PD 08-JUN-2000.
 XX PR XX
 XX PI Herrman R, Wong JF, Lu AL, Presnail JK, Lee J;
 XX DR WPI; 2000-422976/36.
 XX DR P-PSDB; AAY99586.
 XX PT New nucleic acid fragment encoding a scorpion toxin that is a potassium channel agonist, useful for creating transgenic plants that are more insect-tolerant.
 XX PS Claim 2; Page 41; 44pp; English.
 CC The present sequence encodes the scorpion potassium channel agonist Charybdotoxin. The toxin forms a compact structure kept rigid by three disulphide bonds. Potassium channels modulate a number of cellular events such as muscle contraction, neuro-endocrine secretion, frequency and duration of action potentials, electrolyte homeostasis and resting membrane potential. The agonist has a high affinity for the channel and may therefore act by producing an irreversible blockade of the channel. The nucleotide sequence was isolated from clone 1st-ph0011 d2 of a cDNA library representing mRNAs from Leirus scorpion telson tissues. The toxin is insecticidal and the cDNA sequence can therefore be used to create transgenic plants that express the toxin as a means of insect pest control. The amino acid sequence of the present toxin shows homology to the sequence of charybdotoxin from Leirus quinquestriatus (AAY99586)
 XX Sequence 150 BP; 43 A; 23 C; 37 G; 47 T; 0 U; 0 Other;
 CC Alignment Scores:
 CC Pred. No.: 0.148
 CC Score: 77.00
 CC Percent Similarity: 50.00%
 CC Best Local Similarity: 43.33%
 CC Query Match: 28.95%
 CC DB:
 XX US-10-614-934-14 (1-45) x AAA48435 (1-150)
 QY 15 CYSAASnAsnSerGlyGluCysBileProHisCys1leArgileTyAsnThrArgAlaAla 34
 DB 58 TGTACTACATCTAAAGAATGTTGGTGGTTGTGAGACATTGTATAAGACCACAGAGGA 117
 QY 35 LYSCysIleAlaLysThrCysAsnCysTyr 44
 DB 118 AAGTGATGATAATAAATGCCGCTGTAT 147
 RESULT 11
 ID AAF27530
 ID AAF27530 standard; DNA; 176 BP.
 XX AC AAF27530;
 XX DT 28-MAR-2001 (first entry)
 DE Scorpion potassium channel blocking toxin 15-1 DNA.
 XX RW Scorpion; toxin; K-channel; potassium; insect; pesticide; ds.
 XX OS Hottentotta judaica.
 XX PN WO200078958-A2.
 XX PD 28-DEC-2000.
 XX PR XX
 XX PR 21-JUN-2000; 2000WO-US017049.
 XX PR 22-JUN-1999; 99US-0140227P.
 XX PR XX

PT proteins for production e.g. of insect-tolerant transgenic plants for controlling insect pest damage and parasitic worm infections.

XX

PS Claim 1; Page 47; 50pp; English.

XX The present invention relates to scorpion toxins. The invention may be used for the creation of transgenic plants which express K-channel modifers, useful as a means for controlling insect pests by producing insect-to tolerant plants. In the prevention and/or treatment of insect pest damage and parasitic worm infections in animals and humans, the invention may also find use in creating specific new pesticides and anti-helmintic drugs that are also non-toxic to humans, pets and livestock

CC Sequence 177 BP; 61 A; 22 C; 31 G; 63 T; 0 U; 0 Other;

CC

CC Alignment Scores:

Pred. No.:	1.16	Length:	177
Score:	71.00	Matches:	13
Percent Similarity:	52.94%	Conservative:	5
Best Local Similarity:	38.24%	Mismatches:	16
Best Local Similarity:	26.69%	Indels:	0
Query Match:	4	Gaps:	0

DB: US-10-614-934-14 (1-45) x ADR13786 (1-435)

DB: QY 11 IleAsnTyraArgCysAsnAsnSerGlyGluCysileProHisCysIleArgileTyraAsn 30
73 ATAGACCTAAATGTTATTCATCTAACATGTGATGTTGCTGAAAAGTAACTGGGA 132

Db: QY 31 ThrArgAlaLalaLysCysIleAsnAsnLysThrCysAsnCysTyr 44
133 CGGTTCAAGGAAATGCCAGATAAACATGCGCGTAT 174

Db: RESULT 15 ABN60476/C
ID ABN60476 standard; cDNA; 598 BP.

DB: AC ABN60476;
XX DT 28-JUN-2002 (first entry)
XX DE Human cancer related polynucleotide SEQ ID NO 443.
XX PR 16-AUG-2000; 2000US-0226326P.
XX PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX PI Escobedo J, Garcia PD, Sudduth-Klinger J, Reinhard C, Randazzo F;
PI Lamson G, Scott EM, Zhang G, Kassem A, Pot D, Labat I;
XX DR WPI; 2002-24105/29.

PD 17-APR-2002.
XX 12-OCT-2001; 2001CN-00131909.
XX PR 12-OCT-2001; 2001CN-00131909.

PA (JIYY/) JI Y.
XX PI Ji Y, Li Y, Ye J;

XX DR WPI; 2002-509500/55.
DR P-PSB, ADR13780, ADD13781, ADR13790.

PS Martentoxin as one great-conductance calcium-activating potassium channel blocker and its preparation.

PS Disclosure; SEQ ID NO 7; 30pp; Chinese.

XX The invention comprises the amino acid coding sequence of a Chinese scorpion martentoxin peptide. The martentoxin peptide of the invention is useful as a potassium channel blocker. The present DNA sequence encodes the Chinese scorpion martentoxin peptide of the invention.

XX Sequence 435 BP; 148 A; 51 C; 67 G; 169 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	7.38	Length:	598
Score:	70.00	Matches:	17
Percent Similarity:	50.98%	Conservative:	9

SQ Sequence 598 BP; 232 A; 111 C; 134 G; 121 T; 0 U; 0 Other;

Best Local Similarity: 33.33% Mismatches: 13
Query Match: 26.32% Indels: 12
DB: 6 Gaps: 4

US-10-614-934-14 (1-45) x ABN60476 (1-598)

Qy 5 CysGlyGlyGlynlystysIle---AsnTyrArgCysSerSerCysCysIlePro 23
Db 168 TGTCTGGCCCTTCAAAGTGCTGGATTACGGTGTGAGCCCTG-----TGTCCTGAC 115

Qy 24 HisCysIleAlaGlyLeuGlyTyrAsnThrArgGalaLysCys-----IleAsn 38
Db 114 TACTGCACTGTTTCACAGCTACTCTAGTTAACATGCACACTTCATGAAATACA 55

Qy 39 AspThr-Cys-----AsnCysTyrPro 45
Db 54 GAGACTTGCAAAAGCTTAATTCTGTATCT 22

Search completed: August 19, 2005, 05:11:53
Job time : 436 secs

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Om protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 04:24:18 ; Search time 3109 Seconds
(without alignments)
550.945 Million cell updates/sec

Title:	US-10-614-934-14
Sequence:	MMFQCQGKQKINRKCNCNISGE.....IRIYINTRAKACNKTCNCYP 45
Scoring table:	BLOSUM62
Xgapop	10.0 , Xgapext 0.5
Ygapop	10.0 , Ygapext 0.5
Fgapop	6.0 , Fgapext 7.0
Delop	6.0 , Delext 7.0
Searched:	34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters:	68479088
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1P
-Q=cgn2_1.USPTO_spool.p US1064934/runat_17082005_181357_22105/app_query.fasta_1.199
-DB=BST -SFT=fratcat -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-OUTFILE=ptc -NOIN=ext -HEAPSIZEMAX=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US1061434 @CGN_1_1_510 @runat_17082005_181357_22105 -NCPU=6 -MODE=LOCAL
-DOCALLIGN=0 -THR SCORE=0.05 -THR MAX=1000 -THR MIN=100 -ALIGNS=10 -XGAPO=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7
-FGAPEXT=7 -YGAPO=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_htc:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gb81:
9: gb_gb82:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
B0033213/c	526	526 bp	B0033213	mRNA linear EST 27-MAR-2-2002
DEFINITION	UT-1-CFO-axp-g-12-0-UT.s1 NCI_CGAP_P171 Mus musculus cDNA clone			
LOCUS	526 bp mRNA linear EST 27-MAR-2-2002			
ACCESSION	UT-1-CFO-axp-g-12-0-UT 3', mRNA sequence.			
VERSION	B0033213			
KEYWORDS	B0033213.1 GI:19768492			
SOURCE	EST: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
ORGANISM	Mus musculus (house mouse)			
Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1. (bases 1 to 526) NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
AUTHORS	Unpublished (1997)			
TITLE	Contact: Robert Strausberg, Ph.D.			
JOURNAL	Email: cgaps@mail.nih.gov			
COMMENT	Tissue procurement: Dr. Minoru Ko, Dr. Janet Rossent, Dr. Janet Rosset			
FEATURES	cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu The following repetitive elements were found in this cDNA sequence: 1-27, >AT-rich#Low complexity 33-257, >ME67B#UTR/MER4#group (matched complement) Seq. Primer: M13 FORWARD POLY=A:Yes Location/Qualifiers			
source	1. .526			

COMMENT	Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rci.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rci.riken.jp
/mol_type="mRNA"	
/strain="CS7BL/6J"	
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/clone="UI-1-CFO-apx-g-12-0-UI"	
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/lab_host="DHLOB (Life Technologies)"	
/clone_lbi="NCI CGAP PITr1"	
/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: BCO RI; Site 2: Not I; NCI CGAP PITr1 is a subtracted cDNA library constructed according to Bonaldo, Leonor and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) ₁₈ tail. The sequence tags for this library are GTCG, ATCAT, GGGTG, GGTC. For additional information, contact: Bento Soares, bento-soares@uic.edu	
TAG TISSUE=placenta mouse 11.5-12.5 days	
TAG LIB=UI-1-CFO	
TAG SEQ=ATCAT"	
ORIGIN	
Alignment Scores:	
Pred. No.: 2.94	Length: 526
Score: 79.50	Matches: 16
Percent Similarity: 47.73%	Conservative: 5
Best Local Similarity: 36.36%	Mismatches: 20
Query Match: 29.89%	Indels: 3
DB: 5	Gaps: 1
US-10-614-934-14 (1-45) x BQ033213 (1-526)	
QY	4 PheCygGlnGlyGlnlysylsleAlaTyrargCysAsnAsnSer-----GlyGlu 20
Db	151 TTTCCTCCAGAACAGAAACGCCCTCTTGAAATCATCAAAAATTGTGCGTC 92
QY	21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db	91 TGTTCATTCATTTGTTGGGAAGATAATAATGCCATCTCTATAATTGCCAACTAGTAAT 32
QY	41 CysAsnCysTyr 44
Db	31 TGTAAATGCTTT 20
RESULT 2	
AG50152/c	
LOCUS AG50152	765 bp DNA linear GSS 04-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-408G22.T7, genomic survey sequence.	
ACCESSION AG50152	
VERSION AG50152.1	GI:48213565
KEYWORDS GSS.	
SOURCE Mus musculus molossinus	
ORGANISM Mus musculus molossinus	
REFERENCE Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.	
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.	
TITLE BAC end Sequences of Library MSMg01	
JOURNAL Unpublished	
REFERENCE 2 (bases 1 to 765)	
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.	
TITLE Direct Submission	
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp URL: http://hgcp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170)	
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	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/db_xref="TAXON:10090"
	/clone="MHPN16p23"
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ORIGIN	
Alignment Scores:	
Pred. No.: 4.66	Length: 766
Score: 79.50	Matches: 16
Percent Similarity: 47.73%	Conservative: 5
Best Local Similarity: 36.36%	Mismatches: 20
Query Match: 29.89%	Indels: 3
DB: 9	Gaps: 1
US-10-614-934-14 (1-45) x AG50152 (1-766)	
QY	4 PheCysGlnGlyGlnlysylsleAlaTyrargCysAsnAsnSer-----GlyGlu 20
Db	342 TTTCCTCCAGAACAGAAACGCCCTCTTGAAATCATCAAAAATTGTGCGTC 283
QY	21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db	282 TGTTCATTCATTTGTTGGGAAGATAATAATGCCATCTCTATAATTGCCAACTAGTAAT 223
QY	41 CysAsnCysTyr 44
Db	222 TGTAAATGCTTT 211
RESULT 3	
CR177814/c	
LOCUS CR177814	840 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN416p23, genomic survey sequence.	
ACCESSION CR177814	
VERSION CR177814.1	GI:4995663
KEYWORDS GSS, genome survey sequence; MICER.	
SOURCE Mus musculus (house mouse)	
ORGANISM Mus musculus	
REFERENCE 1 (bases 1 to 840)	
AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jokkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.	
TITLE Direct Submission	
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK http://www.sanger.ac.uk/MICER	
FEATURES source	
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ORIGIN

Alignment Scores:
 Pred. No.: 5.22 Length: 840
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

RESULT 5
 CR245225/c
 LOCUS CR245225 forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN98106, genomic survey sequence.
 DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN98106, genomic survey sequence.

ACCESSION CR245225
 VERSION CR245225.1 GI:50024079
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
 REFERENCE 1 (bases 1 to 865)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER
 FEATURES Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:00900"
 /clone_lib="MHPN"

RESULT 4
 BX977811/c
 LOCUS BX977811 850 bp DNA linear GSS 05-JUL-2004
 DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN33h07, genomic survey sequence.
 ACCESSION BX977811
 VERSION BX977811.1 GI:49709234
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 850)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER
 FEATURES Location/Qualifiers 1..850
 source /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN33h07"
 /clone_1id="MHPN"
 /clone_1lib="MHPN"

ORIGIN

Alignment Scores:
 Pred. No.: 5.3 Length: 850
 Score: 79.50 Matches: 16
 Percent Similarity: 47.73% Conservative: 5
 Best Local Similarity: 36.36% Mismatches: 20
 Query Match: 29.89% Indels: 3
 DB: 9 Gaps: 1

RESULT 5
 CR245225/c
 LOCUS CR245225 forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN98106, genomic survey sequence.
 DEFINITION Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN98106, genomic survey sequence.

ACCESSION CR245225
 VERSION CR245225.1 GI:50024079
 KEYWORDS GSS; genome survey sequence; MICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.
 REFERENCE 1 (bases 1 to 865)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. http://www.sanger.ac.uk/MICER
 FEATURES Location/Qualifiers 1. .874
 source /organism="Mus musculus"

Alignment Scores:
Qy /db_xref="Taxon:10090"
Db: /clone_lib="MPN"
ORIGIN

Alignment Scores:	Length:	Mismatches:
Pred. No.: 5.48	874	12
Score: 79.50	Matches: 16	Indels: 2
Percent Similarity: 47.73%	Conservative: 5	Gaps: 1
Best Local Similarity: 36.36%	Mismatches: 20	
Query Match: 29.89%	Indels: 3	
Db: 9	Gaps: 1	

US-10-614-934-14 (1-45) x CR257546 (1-874)

Qy 4 PheCysGlyGlyGlnLysylsileAsnTyrArgCysAsnSer-----GlyGlu 20
Db: 782 TTTCTCCAGGACAGAAAGCCTTCCTTGAAATGAAATCAAAATTGCGTC 723

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThr 40
Db: 722 TGTTCGCCATTTCGTGGAGATAATCCATCTCTTAAATTGCCAACTGTAAT 663

Qy 41 CysAsnCysTyr 44
Db: 662 TGTAAATGCTT 651

RESULT 7
LOCUS CK173729 769 bp mRNA linear EST 01-JUL-2004
DEFINITION EST63049 BEA Boophilus microplus cDNA clone BEAA765, mRNA
ACCESSION CK173729
VERSION GI:49554268
KEYWORDS
SOURCE Boophilus microplus (southern cattle tick)
ORGANISM Boophilus microplus
REFERENCE Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodoidea; Boophilidae; Boophilus.
AUTHORS 1 (bases 1 to 769)
TITLE An index of genes transcribed in the tick Boophilus microplus
JOURNAL Unpublished (2004)
COMMENT Other ESTs: EST63048
CONTACT: Vishwanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0098
Email: nene@tigr.org
Seq primer: M13 reverse.
FEATURES
source
Location/Qualifiers
1. .769 /organism="Boophilus microplus"
/mol_type="mRNA"
/db_xref="taxon:6941"
/clone="BEAA765"
/dev_stage "adult and larva"
/lab_host="E. coli strain DH10B-Tn1"
/clone_lib="BEA"
/note="Organ: Whole ticks and dissected organs; vector: pExpress 1; A normalized cDNA library was custom built by Express Genomics. Oligo-dT primed cDNA was directionally cloned into Not-I-PcRV site of pExpress 1. Universal M13 primers were used to generate 5' and 3' EST data."
ORIGIN

Alignment Scores:	Length:	Mismatches:
Pred. No.: 35.6	794	12
Score: 73.00	Matches: 13	Indels: 2
Percent Similarity: 50.09%	Conservative: 13	Gaps: 1
Best Local Similarity: 29.55%	Mismatches: 16	
Query Match: 27.44%	Indels: 2	
Db: 9	Gaps: 2	

US-10-614-934-14 (1-45) x AG586472 (1-794)

RESULT 8
LOCUS AG586472/c 794 bp DNA linear GSS 05-JUN-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-513N13.TJ, genomic survey sequence.
ACCESSION AG586472
VERSION AG586472.1 GI:48347302
KEYWORDS GSS.
ORGANISM Mus musculus molossinus
MAMMALIA; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE BAC end Sequences of Library MSMg01
JOURNAL Unpublished (bases 1 to 794)
COMMENT 2 (bases 1 to 794)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuninya Abe (abe@rci.riken.jp). Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170).
The Institute of Physical and Chemical Research (RIKEN) 3-1-1, Tsukuba Institute, Bio Resource Center, Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 mail: abe@rci.riken.jp
PRIMERS
SEQUENCING : TJ
LIBRARY
source
Location/Qualifiers
1. .794 /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/db_xref="taxon:57466"
/clone="MSMg01-513N13.TJ"
/sex="male"
/tissue_type "mixture of kidney and spleen"
/Clone_Id="MSMg01 Mouse Male BAC Library"

ORIGIN

Alignment Scores:	Length:	Mismatches:
Pred. No.: 35.6	794	12
Score: 73.00	Matches: 13	Indels: 2
Percent Similarity: 50.09%	Conservative: 13	Gaps: 1
Best Local Similarity: 29.55%	Mismatches: 16	
Query Match: 27.44%	Indels: 2	
Db: 9	Gaps: 2	

US-10-614-934-14 (1-45) x AG586472 (1-794)

/clone lib="Cv Hemo Hypoxia Forw SSH" /note="Vector; PCR2.1; Site_1: none; Site_2: none"

ORIGIN	DEFINITION	LOCATION	DEFINITION	LOCATION
Alignment Scores:				
Pred. No.: 15	17.4	Length: 345	est c virginica546 Cv Hemo 4hr Immune Reverse SSH Crassostrea	CV087806/c
Score: 72.00		Matches: 11	est c virginica CDNA, mRNA sequence.	
Percent Similarity: 55.17%		Conservative: 5		
Best Local Similarity: 37.93%		Mismatches: 9		
Query Match: 27.07%		Indels: 4		
DB: 7		Gaps: 1		
RESULT 12				
US-10-614-934-14 (1-45) x CV087280 (1-345)				
LOCUS CV087696				
DEFINITION est c virginica817 Cv Hepato Cadmium Forward SSH Crassostrea				
REFERENCE 15 CyasnanserGlyGluCysileProHisCysileArgileTyrAsnThrArgAlaala 34				
ACCESSION CV087696				
JOURNAL TGCACACAGATCTGATGTCGCCACTGC-----GACCCACATTCTGGA 73				
KEYWORDS				
SOURCE 35 LysCysIleAsnLySThrCysAsnCys 43				
ORGANISM 72 ACTGTATCACACCAACGCACTGT 46				
Crassostrea virginica (eastern oyster)				
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreida;				
Ostroidea; Ostreidae; Crassostrea.				
REFERENCE 1 (bases 1 to 345)				
AUTHORS Jenny.M.J., Warr.G.W., Gross.P.S., Almeida.J.S., Chen.Y., McKillen.D.J., Wu.S. and Chapman.R.W.				
TITLE Crassostrea virginica EST Library at marinegenomics.org				
COMMENT Unpublished (2004)				
CONTACT: Gross PS				
Medical University of South Carolina				
Box 250509, 173 Ashley Avenue, Charleston, SC 29425, USA				
Tel: 843 792 8503				
Fax: 843 792 4850				
EMAIL: grossp@musc.edu				
FEATURES location/Qualifiers				
source 1 .345				
/organism="Crassostrea virginica"				
/mol_type="mRNA"				
/db_xref="taxon:6565"				
/cell_type="Hemocyte"				
/clone lib="Cv Hemo 4hr Immune Reverse SSH" /note="Vector; PCR2.1; Site_1: none; Site_2: none"				
ORIGIN				
Alignment Scores:				
Pred. No.: 15	17.4	Length: 345	345 bp mRNA linear EST 26-AUG-2004	RESULT 13
Score: 72.00		Matches: 11		
Percent Similarity: 55.17%		Conservative: 5		
Best Local Similarity: 37.93%		Mismatches: 9		
Query Match: 27.07%		Indels: 4		
DB: 7		Gaps: 1		
RESULT 14				
US-10-614-934-14 (1-45) x CV087806 (1-345)				
LOCUS CB018045				
DEFINITION pgnc_pk018_012 Chicken lymphoid cDNA library (pgnc) Gallus gallus				
REFERENCE 15 CyasnanserGlyGluCysileProHisCysileArgileTyrAsnThrArgAlaala 34				
ACCESSION CB018045				
JOURNAL (pLdg(P) 4), mRNA sequence.				
KEYWORDS CB018045.1 GI:27592781				
EST.				
SOURCE Gallus gallus (chicken)				
ORGANISM Gallus gallus				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
REFERENCE 1 (bases 1 to 623)				
AUTHORS Morgan.R.W. and Burnside.J.				
TITLE Chicken ESTs from lymphoid tissue				
COMMENT Unpublished (2002)				
CONTACT: Robin.W. Morgan				
University of Delaware				
Db 225 TGCACACAGATCTGATGTCGCCACTGC-----GACCCACATTCTGGA 273				
Qy 35 LysCysIleAsnLySThrCysAsnCys 43				
Db 274 ACTGTATCACACCAACGCACTGT 300				

Townsend Hall, Newark, DE 19717, USA

Tel: 302-831-1341

Fax: 302 831-2822

Email: morgan@udel.edu, www.chickest.udel.edu.

FEATURES source

Location/Qualifiers
1. .623

/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"

/clone="pgn1c_pk018_012"

/box="Male and Female"

/tissue_type="thymus, burse, spleen, PBL, bone marrow"

/lab_host="E. coli EMH10B"
/clone_lib="Chicken lymphoid cDNA library (pgn1c)"

/note="Vector: pCMVSPORT 6"

ORIGIN

Alignment Scores:

Pred. No.: 35.9

Length: 623

Score: 72.00

Percent Similarity: 46.81%

Matches: 17

Conservative: 5

Best Local Similarity: 36.17%

Mismatches: 11

Query Match: 27.07%

Indels: 14

Gaps: 3

US-10-614-934-14 (1-45) x CB018045 (1-623)

Qy 11 IleAsnTyrArgCysAsnAsnSerCysGlu-----Cys 21

Db 223 ATTGACACTATGTATAGAGGGTTCTCTAAATCAGGCAGCCGTTGGGGCGCTT 282

Qy 22 IleProHisCysIleArgIleTyrAsnThrArgAlaAlaLysCysIleAsnLysThrCys 41

Db 283 ATGCTTCACAGCAGGAGGTATAAT----GCCGAAATGTTACCTCATATTGT 336

Qy 42 AsnCys-----TyrPro 45

Db 337 TACTGTGGATGTGATTACCA 357

ORIGIN

Alignment Scores:

Pred. No.: 61.6

Length: 967

Score: 72.00

Percent Similarity: 61.29%

Best Local Similarity: 45.16%

Matches: 14

Conservative: 5

Mismatches: 8

Indels: 4

Gaps: 1

US-10-614-934-14 (1-45) x BG420272 (1-967)

Qy 3 IlePheCysGlnGlyGlnLysValLeuAsnTyrArgCysAsnAsnSerCysIle 22

Db 780 ATTTCCTGTAATGGTGAAATGAACITATCGATGAGGGCCACAACCTCTGGTAC---- 727

Qy 23 ProHisCysIleArgIleTyrAsnThrArgAla 33

Db 726 -----TGTGTGTCGTTTCATACACACGGCA 700

Search completed: August 19, 2005, 06:33:27

Job time : 3114 secs

/tissue_type="renal cell adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 14"

/note="Organ: kidney; Vector: pOTB7; Site 1: XbaI; site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using 5'

adaptor: GCGACGAG (G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and SuperScript II RT (Life Technologies)."

FEATURES source

Location/Qualifiers
1. .967

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4586972"

FEATURES source

Location/Qualifiers
1. .967

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4586972"

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model.
Run on: August 19, 2005, 10:20:42 ; Search time 131 Seconds
(without alignments)
562.080 Million cell updates/sec

Title: US-10-614-934-14
Perfect score: 266

Sequence: 1 MMIFCQCKKINYRCNNSGE.....IRIYNTRAAKCIKTCNCYP 45

Scoring table: BLOSUM62
Xgapext 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 122784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2_1/US710/spool/P/US10614934/runat_19082005_112037_24047/app_query.fasta_1.199

-LOOPEXT=0 -UNITS=5ts -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=10CT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=PTO -NORMEXT -HEARPIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10614934 @CGN_1_1_105 @runat_19082005_112037_24047 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEGS SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV -TIMOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A/COMB.seq:#
2: /cgn2_6/prodata/1/ina/5B/COMB.seq:#
3: /cgn2_6/prodata/1/ina/6A/COMB.seq:#
4: /cgn2_6/prodata/1/ina/6B/COMB.seq:#
5: /cgn2_6/prodata/1/ina/PCtUS/COMB.seq:#

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	266	100.0	138	US-09-857-401B-13 Sequence 13, Appli
2	101	38.0	114	US-09-857-401B-9 Sequence 9, Appli
3	92.5	34.8	186	4 US-10-044-59-3 Sequence 3, Appli
4	91.5	154	1	US-08-096-942-5 Sequence 5, Appli
5	91.5	34.4	154	5 PCT-US4-0863-5 Sequence 5, Appli
6	87.5	32.9	180	4 US-10-044-59-5 Sequence 5, Appli
7	86.5	32.5	120	1 US-08-096-942-2 Sequence 2, Appli
8	86.5	32.5	174	4 US-10-044-339-19 Sequence 19, Appli
9	78	29.3	180	4 US-09-857-401B-15 Sequence 15, Appli
10	77	28.9	150	4 US-09-857-401B-11 Sequence 11, Appli
11	75	28.2	176	4 US-10-044-339-15 Sequence 15, Appli
12	27.4	177	4	US-09-857-401B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-857-401B-13 ; Sequence 13, Application US/09857401B

Patent No. 6593141 ; GENERAL INFORMATION:

APPLICANT: HERRMANN, RAFAEL

APPLICANT: WONG, JAMES F.

APPLICANT: LU, ALBERT L.

APPLICANT: PRESVAIL, JAMES K.

APPLICANT: LEE, JIAN-MING

TITLE OF INVENTION: SCORPION TOXINS

FILE REFERENCE: BB1102

CURRENT APPLICATION NUMBER: US/09/857,401B

PRIOR APPLICATION NUMBER: 60/110,590

PRIOR FILING DATE: 1998-12-02

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Microsoft Office 97

SEQ ID NO: 13

LENGTH: 138

TYPE: DNA

ORGANISM: Leirurus quinquestrigatus

US-09-857-401B-13

Alignment Scores:
Pred. No.: 3.58e-29
Score: 266.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%

Query Match: 4
DB: 4

Gaps: 0

Length: 138
Matches: 45
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

Sequence 17, Appli
Sequence 2, Appli
Sequence 11817, A
Sequence 15439, A
Sequence 5432, Ap
Sequence 20714, A
Sequence 51773, A
Sequence 12872, A
Sequence 13239, A
Sequence 7, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 15220, A
Sequence 11808, A
Sequence 13388, A
Sequence 12401, A
Sequence 18, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 46, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 1018, Ap
Sequence 418, Ap
Sequence 418, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 982, Ap
Sequence 15221, A
Sequence 25, Appli

Db 1 ATGATGATTCTGCCAAGCCAGAAAAATAATTATCGATGTAATAACGGTAG 60
 QY 21 CysileProlisCysileArgileTyramylThrArgAlaLalaLysCysteAsnlySthr 40
 Db 61 TGATTCACATGATCAGATAATAACCAAGCAGCAGTGTAAACCA 120
 QY 41 CysanCYSyPro 45
 Db 121 TGCATGTTATCCA 135

RESULT 2
 US-09-857-401B-9
 ; Sequence 9, Application US/09857401B
 ; GENERAL INFORMATION:
 ; APPLICANT: HERRMANN, RAFAEL
 ; APPLICANT: WONG, JAMES F.
 ; APPLICANT: LU, ALBERT L.
 ; APPLICANT: PRASSNAIL, JAMES K.
 ; APPLICANT: LEE, JIAN-MING
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1102
 ; CURRENT APPLICATION NUMBER: US/09/857,401B
 ; PRIORITY FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 9
 ; LENGTH: 114
 ; TYPE: DNA
 ; ORGANISM: Leiuurus quinquestriatus
 ; US-09-857-401B-9

Alignment Scores:
 Pred. No.: 4.63e-06 Length: 114
 Score: 101.00 Matches: 17
 Percent Similarity: 58.82% Conservative: 3
 Best Local Similarity: 50.00% Mismatches: 14
 Query Match: 37.97% Indels: 0
 DB: Gaps: 4

US-10-614-934-14 (1-45) × US-10-044-359-3 (1-186)
 RESULT 4
 US-08-096-942-5
 ; Sequence 5, Application US/08096942
 ; GENERAL INFORMATION:
 ; PATENT NO. 5498895
 ; APPLICANT: GARCIA, MARIA I
 ; APPLICANT: KOO, GLORIA C
 ; APPLICANT: LEONARD, REID J
 ; APPLICANT: LIN, CHIU-CHUAN S
 ; APPLICANT: SLAUGHTER, ROBERT S
 ; APPLICANT: STEVENS, SCOTT P
 ; APPLICANT: WILLIAMSON, JOANNE M
 ; TITLE OF INVENTION: SCORPION PEPTIDE WITH IMMUNOSUPPRESSANT
 ; TITLE OF INVENTION: ACTIVITY
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CATHERINE A. DOLAN, MERCK & CO., INC.
 ; STREET: P.O. BOX 2000, 126 LINCOLN AVENUE
 ; CITY: RAILWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07055-0907

QY 12 AsnytRArgCysasnAsnserglGluCysileArgileTyramylThrArgAlaLalaLysCysteAsnlySthr 31
 Db 10 ATGTCGCCGCGAACATCTGGACATGTCGTCAGTTGATCAAAGAGTAATAAT 69

QY 32 ArglaAlaIysCysileAlanylThrCysasnCYSyPro 45
 Db 70 ATAGGGGAAGATGCTGTAATGACAATGTTATGTTATCCA 111

RESULT 3
 US-10-044-359-3
 ; Sequence 3, Application US/10044359
 ; PATTERN NO. 6740743
 ; GENERAL INFORMATION:
 ; APPLICANT: Hermann, Rafael
 ; APPLICANT: Wong, James F.
 ; APPLICANT: Lee, Jian-Ming
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1367 US NA
 ; CURRENT APPLICATION NUMBER: US/10/044,359
 ; CURRENT FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 09/1599,416
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 60/140,227
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 3
 ; LENGTH: 186
 ; TYPE: DNA

US-08-096-942-5
 ; ORGANISM: Hottentotta judaica
 ; US-10-044-359-3
 ; ALIGNMENT SCORES:
 ; PRED. NO.: 0.000142 LENGTH: 186
 ; SCORE: 92.50 MATCHES: 17
 ; PERCENT SIMILARITY: 50.00% CONSERVATIVE: 6
 ; BEST LOCAL SIMILARITY: 36.96% MISMATCHES: 22
 ; QUERY MATCH: 34.77% INDELS: 1
 ; DB: GAPS: 1

QY 1 MetMetIlePheCysGlnGlyGlnLysLysLeAsnTyArgCys---AsnAsnSerGly 19
 Db 45 ATGGTTATTCGAGCCACGCTCATACAGTGATGATGACGATGATGGAGGAGCAGT 105
 QY 20 GluCysileProlisCysileArgileTyramylThrArgAlaLalaLysCysileAsnlySthr 39
 Db 106 AATGGCGAAACCATGCTATGATAAATACGGCACACTAAACTAATGCTCACCAT 165
 QY 40 ThrcysanCYSyPro 45
 Db 166 CGGTGCAACTGTTATCCG 183

Db 85 ||||:||||| ::||| ||||| :||| ||||| ||||| Db 85 ||||:||||| ::||| ||||| :||| ||||| ||||| 144
; Sequence 11, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 11
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Leiuurus quinquestriatus
; US-09-857-401B-11

Alignment Scores:
Pred. No.: 0.0382 Length: 176
Score: 75.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 28.20% Index: 0
DB: 4 Gaps: 0

RESULT 10
US-09-857-401B-11
; Sequence 11, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 11
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Leiuurus quinquestriatus
; US-09-857-401B-11

Alignment Scores:
Pred. No.: 0.0161 Length: 150
Score: 77.00 Matches: 13
Percent Similarity: 50.00% Conservative: 2
Best Local Similarity: 43.33% Mismatches: 15
Query Match: 28.95% Index: 0
DB: 4 Gaps: 0

RESULT 11
US-10-614-934-14 (1-45) x US-09-857-401B-11 (1-150)
; Sequence 15, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO: 15
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Hottentotta judaica
; US-10-044-359-15

Alignment Scores:
Pred. No.: 0.0382 Length: 176
Score: 75.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 28.20% Index: 0
DB: 4 Gaps: 0

RESULT 12
US-10-614-934-14 (1-45) x US-10-044-359-15 (1-176)
; Sequence 1, Application US/09857401B
; Patent No. 6593141
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/09/857,401B
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 1
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Leiuurus quinquestriatus
; US-09-857-401B-1

Alignment Scores:
Pred. No.: 0.0736 Length: 177
Score: 73.00 Matches: 14
Percent Similarity: 45.00% Conservative: 4
Best Local Similarity: 35.00% Mismatches: 22
Query Match: 27.44% Index: 0
DB: 4 Gaps: 0

RESULT 13
US-10-614-934-14 (1-45) x US-09-857-401B-1 (1-177)
; Sequence 17, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Herman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO: 15
; LENGTH: 176
; TYPE: DNA
; ORGANISM: Hottentotta judaica
; US-10-044-359-15

Alignment Scores:
Pred. No.: 0.0382 Length: 176
Score: 75.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 28.20% Index: 0
DB: 4 Gaps: 0

Fri Aug 19 10:52:13 2005

us-10-614-934-14.rni

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GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM protein - nucleic search, using frame_plus_p2n model
Run on: August 19, 2005, 03:05:35 ; Search time 622 Seconds
(Without alignments)
470.034 Million cell updates/sec

Title: US-10-614-934-14
Perfect score: 266
Sequence: 1 MMIFCQGOKKINYRCNNNSGE.....IRINTPAAKCKINKTCNCYP 45

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2_1/USPDB_spool_P1US10614934/runat_17082005_181355_22021/app_query.fasta_1.199
-DBs=Published_Applications_NA -QFMW=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOCCLL=0 -LODDEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40_cdi -LIST45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGNN=15 -MORE=LOCAL -OUTFMT_PTO -NORMEXT -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10614934 @CGN 1.1 .723 @runat_17082005_181355_22021
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPBEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

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9: /cgn2_6/prodata1_1/pubpna/US09B_PUBCOMB.seq:*
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15: /cgn2_6/prodata1_1/pubpna/US10D_PUBCOMB.seq:*
16: /cgn2_6/prodata1_1/pubpna/US10E_PUBCOMB.seq:*
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20: /cgn2_6/prodata1_1/pubpna/US10I_PUBCOMB.seq:*
21: /cgn2_6/prodata1_1/pubpna/US10J_PUBCOMB.seq:*
22: /cgn2_6/prodata1_1/pubpna/US10K_PUBCOMB.seq:*
23: /cgn2_6/prodata1_1/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/prodata1_1/pubpna/US11B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a

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2	101	38 0	114	21	US-10-614-934-9	Sequence 9, Appl
3	92.5	34 8	186	13	US-10-044-359-3	Sequence 3, Appl
4	87.5	32 9	180	13	US-10-044-359-5	Sequence 5, Appl
5	86.5	32.5	174	13	US-10-044-359-19	Sequence 19, Appl
6	79.5	29 9	231	9	US-09-728-44-356	Sequence 356, Appl
7	78	29 3	180	21	US-10-614-934-15	Sequence 15, Appl
8	77	28 9	150	21	US-10-614-934-11	Sequence 11, Appl
9	75	28 2	176	13	US-10-044-359-15	Sequence 15, Appl
10	73	27.4	177	21	US-10-614-934-1	Sequence 1, Appl
11	71.5	26 9	905	18	US-10-425-114-23882	Sequence 17548, A
12	71.5	26 9	1405	18	US-10-614-934-15	Sequence 2882, A
13	71.5	26 9	1770	20	US-10-425-115-38932	Sequence 38929, A
14	71.5	26 9	2525	20	US-10-425-115-38929	Sequence 131, App
15	71	26.7	17	13	US-10-044-359-17	Sequence 1, Appl
16	69.5	26.1	3846	19	US-10-437-963-33842	Sequence 33842, A
17	68.5	25.8	73100	19	US-10-319-914-11	Sequence 11, Appl
18	68	25.6	350570	20	US-10-417-375-146	Sequence 556, App
19	66.5	25.0	83009	20	US-10-417-375-146	Sequence 143, App
20	66	24.8	204	21	US-10-721-793-131	Sequence 1, Appl
21	66	24.8	323	21	US-10-721-793-129	Sequence 1, Appl
22	66	24.8	626	13	US-10-027-632-281127	Sequence 281127, Sequence 166133, Sequence 57403, A
23	66	24.8	626	17	US-10-027-632-281127	Sequence 1987, A
24	65.5	24.6	377	10	US-10-425-115-166413	Sequence 1, Appl
25	65	24.4	288	19	US-10-427-963-57403	Sequence 1, Appl
26	65	24.4	316	19	US-10-377-963-57403	Sequence 1, Appl
27	64	24.1	2185	17	US-10-104-047-556	Sequence 4897, AP
28	64	24.1	2422	19	US-10-437-963-4897	Sequence 148, AP
29	64	24.1	42360	19	US-10-367-094-148	Sequence 3, Appl
30	64	24.1	143306	9	US-09-729-920-3	Sequence 3, Appl
31	64	24.1	143306	20	US-10-887-932-3	Sequence 34016, A
32	63.5	23.9	1542	17	US-10-369-493-34016	Sequence 26499, A
33	63.5	23.9	16553	18	US-10-425-114-26499	Sequence 24, Appl
34	63	23.9	50000	21	US-10-106-635-24	Sequence 6792, AP
35	63.5	23.9	366710	20	US-10-17-19-993-6792	Sequence 501, AP
36	63	23.7	533	16	US-10-029-386-5501	Sequence 15307, A
37	63	23.7	671	13	US-10-027-632-15307	Sequence 15308, A
38	63	23.7	671	13	US-10-027-632-15307	Sequence 15307, A
39	63	23.7	671	17	US-10-027-632-15307	Sequence 15308, A
40	63	23.7	671	17	US-10-027-632-15307	Sequence 15308, A
41	63	23.7	891	9	US-09-810-0336B-7	Sequence 7, Appl
42	63	23.7	891	14	US-10-286-264-63	Sequence 21, Appl
43	63	23.7	891	15	US-10-295-403-559	Sequence 559, AP
44	63	23.7	891	17	US-10-225-066A-559	Sequence 2437, AP
45	63	23.7	891	17	US-10-374-780A-2437	Sequence 2437, AP

ALIGNMENTS

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RESULT 1
US-10-614-934-13
; Sequence 13, Application US/10614934
; Publication No. US200504271A1
; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US10/614,934
; CURRENT FILING DATE: 2003-07-08
; PRIORITY FILING DATE: 2001-06-01
; PRIORITY APPLICATION NUMBER: US/09857,401
```

; PRIOR APPLICATION NUMBER: 60/110,590
; PRIOR FILING DATE: 1998-12-02
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 138
; ; ORGANISM: Leiurus quinquestriatus
; US-10-614-934-13

Alignment Scores:
Pred. No.: 1.14e-27 Length: 138
Score: 266.00 Matches: 45
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 21 Indels: 0
DB: Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-13 (1-138)

Qy 1 MetMetIlePheCysGlnGlyGlnIysLysIleAsnTyrArgCys--AsnAsnSerGlyGlu 20
Db 1 ATGATGATTCTTGCAAGGCCAGAAATAAATTAACGGTGTAAATAGGGTAG 60

Qy 21 CysIleProHisCysIleArgIleTyrAsnThrArgAlaLysCysIleAspLysThr 40
Db 61 TGTATTCAGATTCATGCAAGATAATAACACCAGAGCAGCAGAAGTGTAAATAACA 120

Qy 41 CysAsnCystePro 45
Db . 121 TGCATATGTTATCCA 135

RESULT 2
US-10-614-934-9
; Sequence 9, Application US/10614934
; Publication No. US20050042117A1

; GENERAL INFORMATION:
; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 186

TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-3

Alignment Scores:
Pred. No.: 0.00141 Length: 186
Score: 92.50 Matches: 17
Percent Similarity: 50.00% Conservative: 6
Best Local Similarity: 36.96% Mismatches: 22
Query Match: 34.77% Indels: 1
DB: Gaps: 13

US-10-614-934-14 (1-45) x US-10-044-359-3 (1-186)

Qy 1 MetMetIlePheCysGlnGlyGlnIysLysIleAsnTyrArgCys--AsnAsnSerGly 19
Db 46 ATGGTATTCTTGAGCCACGCTCATACGAGTGTGGATGAGCTGATCGAGGAGCAGAT 105

Qy 20 GluCysIleProHisCysIleArgIleTyrAsnThrArgAlaLalLysCysIleAsnLys 39
Db 106 AATGGCTTAACCATGCTATGATAAAACGGCACAACTAAACTAATGCATCAACGAT 165

Qy 40 ThrCysAsnCystePro 45
Db 166 CGGTGCAACTGTATCCG 183

RESULT 4
US-10-044-359-5
; Sequence 5, Application US/10044359
; Publication No. US2002010454A1

; GENERAL INFORMATION:
; APPLICANT: Herman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 180

TYPE: DNA
; ORGANISM: Hottentotta judaica
US-10-044-359-5

Alignment Scores:
Pred. No.: 5.05e-05 Length: 114
Score: 101.00 Matches: 17
Percent Similarity: 58.82% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 14
Query Match: 37.97% Indels: 0
DB: Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-9 (1-114)

Qy 12 AsnTyrArgCysAsnAsnSerGlyGluCysIleProHisCysIleArgIleTyrAsnThr 31
Db 10 ATGGGCCGCGCAAGATTCTGGACATGCTCCAGTTRGCATAAAAGTAATAAT 69

32 ArgAlaAlaLysCysIleAsnLysThrCysAsnCystePro 45

Pred. No.: 0.135 Length: 180
Score: 78.00 Matches: 13
Percent Similarity: 56.67% Conservative: 4
Best Local Similarity: 43.33% Mismatches: 13
Query Match: 29.32% Indels: 0
Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-15 (1-180)

Qy 35 LysCysIleLeuLysThrCysAsnCysTyr 44
Db 145 AGATGTATGATAATGCGCTGTAT 174

RESULT 8

US-10-614-934-11

; Sequence 11, Application US/10614934
; Publication No. US20050042717A1

; GENERAL INFORMATION:

; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; TITLE OF INVENTION: SCORPION TOXINS
; CURRENT APPLICATION NUMBER: US/10/614,934
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/857,401
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO: 11
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Leirusus quinquestriatus
; US-10-614-934-11

Alignment Scores:
Pred. No.: 0.146 Length: 150
Score: 77.00 Matches: 13
Percent Similarity: 50.00% Conservative: 2
Best Local Similarity: 43.33% Mismatches: 15
Query Match: 28.95% Indels: 0
Db: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-11 (1-150)

Qy 15 CysAsnAsnSerGlyGluCysIleArgIleTyrAsnThrArgAlaAla 34
Db 58 TGTACTACATCTAAAGAATGTTGGCTGGTTGTGAGACATTGATAAGACCAAGAGGA 117

RESULT 9

US-10-044-359-15

; Sequence 15, Application US/10044359
; Publication No. US20020160454A1

; GENERAL INFORMATION:

; APPLICANT: Hermann, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1167 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11

Alignment Scores:
Pred. No.: 0.645 Length: 177
Score: 73.00 Matches: 14
Percent Similarity: 45.00% Conservative: 4
Best Local Similarity: 35.00% Mismatches: 22
Query Match: 27.44% Indels: 0
Db: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-1 (1-177)

Qy 5 CysGlyGlyGlnLysIleAsnTyrArgCysAsnSerGlyGluCysIleProH 24
Db 55 TGTAGTGAGCTGACTCATAGCTGATGTTGATCTGTGATGTTGGAAAGCT 114

Qy 25 CysIleArgIleTyrAsnThrArgAlaAlaValCysIleAsnLysThrCysAsnCysTyr 44
Db 115 TGAGAAAGTAGCAGGATUGGGACAAGAAATGCCAGATATCACAGTCCTGCTAT 174

PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO: 15
LENGTH: 176
TYPE: DNA
ORGANISM: Hottentotta judaica
US-10-044-359-15

Alignment Scores:
Pred. No.: 0.34 Length: 176
Score: 75.00 Matches: 13
Percent Similarity: 52.94% Conservative: 5
Best Local Similarity: 38.24% Mismatches: 16
Query Match: 28.20% Indels: 0
Db: 13 Gaps: 0

US-10-614-934-14 (1-45) x US-10-044-359-15 (1-176)

Qy 11 LysLeuTyrArgCysAsnSerGlyGluCysIleArgIleTyrAsn 30
Db 73 ATAGACGTTAGATGATGAGCTCTCTGTTGATGTTGGAAAGCTTGCCAGAAAGTACAGGA 132

Qy 31 ThrArgAlaAlaLysCysIleLeuLysThrCysAsnCysTyr 44
Db 133 TCAGGACAGGAAAGTGCAGATAACCAAATGTCGTTGTTAT 174

RESULT 10

US-10-614-934-1

; Sequence 1, Application US/10614934
; Publication No. US20050042717A1

; GENERAL INFORMATION:

; APPLICANT: HERRMANN, RAFAEL
; APPLICANT: WONG, JAMES F.
; APPLICANT: LU, ALBERT L.
; APPLICANT: PRESNAIL, JAMES K.
; APPLICANT: LEE, JIAN-MING
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BB1102
; CURRENT APPLICATION NUMBER: US/10/614,934
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US/09/857,401
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/110,590
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO: 1
; LENGTH: 177
; TYPE: DNA
; ORGANISM: Leirusus quinquestriatus
; US-10-614-934-1

Alignment Scores:
Pred. No.: 0.645 Length: 177
Score: 73.00 Matches: 14
Percent Similarity: 45.00% Conservative: 4
Best Local Similarity: 35.00% Mismatches: 22
Query Match: 27.44% Indels: 0
Db: 21 Gaps: 0

US-10-614-934-14 (1-45) x US-10-614-934-1 (1-177)

Qy 5 CysGlyGlyGlnLysIleAsnTyrArgCysAsnSerGlyGluCysIleProH 24
Db 55 TGTAGTGAGCTGACTCATAGCTGATGTTGATCTGTGATGTTGGAAAGCT 114

Qy 25 CysIleArgIleTyrAsnThrArgAlaAlaValCysIleAsnLysThrCysAsnCysTyr 44
Db 115 TGAGAAAGTAGCAGGATUGGGACAAGAAATGCCAGATATCACAGTCCTGCTAT 174

RESULT 11 ; FEATURE:
 US-10-425-114-17548 ; OTHER INFORMATION: Clone ID: LIB3606-012-B7_FLI
 Sequence 17548, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovacic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 FILE REFERENCE: 38-21(5331)B
 CURRENT APPLICATION NUMBER: US/10-425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO: 17548
 LENGTH: 905
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: LIB3069-044-A1_FLI
 US-10-425-114-17548

Alignment Scores:
 Pred. No.: 8.48 Score: 71.50 Length: 1405
 Percent Similarity: 34.92% Best Local Similarity: 23.81%
 Best Local Similarity: 23.81% Query Match: 26.88%
 Query Match: 18 DB:
 DB: 18

Length: 905
 Matches: 15
 Conservative: 7
 Percent Similarity: 34.92% Conservativeness: 7
 Best Local Similarity: 23.81% Mismatches: 18
 Query Match: 26.88% Indels: 23
 Gaps: 1

US-10-614-934-14 (1-45) x US-10-425-114-23882 (1-1405)

QY 5 CysGlnGlyGlnLysylAsnTyrArgCysAsparnSerGlyXGlucylsileProHis 24
 Db 826 TGCCAGGCCAGAGGAGATGGATTCTCTCAACCCACTGGAGCTCAAATGGCAC 945

QY 25 Cys----- 25
 Db 886 TGCTGGCGAAGTTGTCAAAGGCCCTCCCCAGAAAATGGATCAACCGGGTCAGTGCGAC 905

QY 26 -----IleargIleTyrasnThrArgAlaAlaIysCysIleAsnlysThrCys 41
 Db 946 GAACATCTCTCGTCAGATCATGTCAGACATTCAAGATGTTCCACCAAGAGAGGTGC 1005

QY 42 AsnCysTyr 44
 Db 1006 GGATGCCAT 1014

RESULT 13 ; FEATURE:
 US-10-425-115-38932 ; OTHER INFORMATION: Clone ID: LIB3606-012-B7_FLI
 Sequence 38932, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovacic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10-425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 38932
 LENGTH: 1770
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_135507C.1
 US-10-425-115-38932

Alignment Scores:
 Pred. No.: 20.1 Score: 71.50 Length: 1770
 Percent Similarity: 34.92% Best Local Similarity: 23.81%
 Best Local Similarity: 23.81% Query Match: 26.88%
 Query Match: 20 DB:
 DB: 20

Length: 1770
 Matches: 15
 Conservative: 7
 Percent Similarity: 34.92% Conservativeness: 7
 Best Local Similarity: 23.81% Mismatches: 18
 Query Match: 26.88% Indels: 23
 Gaps: 1

US-10-614-934-14 (1-45) x US-10-425-115-38932 (1-1770)

QY 5 CysGlnGlyGlnLysylAsnTyrArgCysAsparnSerGlyXGlucylsileProHis 24
 Db 1143 TGCCAGGCCAGAGGAGATGGATTCTCTCAACCCACTGGAGCTCAAATGGCAC 1202

QY 25 Cys----- 25
 Db 1203 TGCTGGCGAAGTTGTCAAAGGCCCTCCCCAGAAAATGGATCAACCGGGTCAGTGCGAC 1262

QY 26 -----IleargIleTyrasnThrArgAlaAlaIysCysIleAsnlysThrCys 41
 Db 1204 TGCTGGCGAAGTTGTCAAAGGCCCTCCCCAGAAAATGGATCAACCGGGTCAGTGCGAC 1262

TYPE: DNA
 ORGANISM: Zea mays

RESULT 12 ; FEATURE:
 US-10-425-114-23882 ; OTHER INFORMATION: Clone ID: LIB3606-012-B7_FLI
 Sequence 23882, Application US/10425114
 Publication No. US20040034888A1
 GENERAL INFORMATION:
 APPLICANT: Liu, Jingdong
 APPLICANT: Zhou, Yihua
 APPLICANT: Kovacic, David K.
 APPLICANT: Screen, Steven E
 APPLICANT: Tabaska, Jack E
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
 FILE REFERENCE: 38-21(5331)B
 CURRENT APPLICATION NUMBER: US/10-425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO: 23882
 LENGTH: 1405
 TYPE: DNA
 ORGANISM: Zea mays

Db 1263 AACATCTCGTCAGATGTCAGACATTCCACAGATGTTCCACAGAGCGTGC 1322 ; SEQ ID NO: 17
 Qy 42 AsnC₈Tyr 44 ; LENGTH: 177
 ; TYPE: DNA
 ; ORGANISM: Hottentotta judaica
 Db 1323 GGATGCCAT 1331 ; US-10-044-359-17
 RESULT 14
 US-10-425-115-38929
 ; Sequence 38929, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILE REFERENCE: 38-21(5322)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO: 38929
 ; LENGTH: 2525
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT457_135504C.1
 US-10-425-115-38929
 Alignment Scores:
 Pred. No.: 31.8 Length: 2525 ; SEQ ID NO: 17
 Score: 71.50 Matches: 71.00 ; LENGTH: 177
 Percent Similarity: 34.92% Conservative: 5
 Best Local Similarity: 23.81% Mismatches: 16
 Query Match: 26.88% Indels: 0
 DB: Gaps: 0
 US-10-614-934-14 (1-45) x US-10-044-359-17 (1-177)
 Qy 11 IleasnTyrArgCysAsnAsnSerGlyGluCysileProHisCysilearginleTyrasn 30
 Db 73 ATAGACGTAAATGTTATTCATCTCAAGATGTTGGATGCTGCTGTAAGAAAGTACTGA 132
 Qy 31 ThrArgAlaAlaLysCysileasnLysThrCysAsnC₈Tyr 44
 Db 133 CGGTTCAAGGAAATGCCAGAAATAACAGATGTCGTAT 174
 Search completed: August 19, 2005, 05:04:30
 Job time : 628 secs

US-10-614-934-14 (1-45) x US-10-425-115-38929 (1-2525)

Qy 5 CysGlyGlyGlnLysIleAsnTyrArgCysAsnAsnSerGlyGluCysileProHis 24
 Db 1842 TGCCAGAGCCGAGAGGAGATTGATTCTCTCAACCCCTGGAGCTCAAATGTGAC 1901
 Qy 25 Cy₈----- ; SEQ ID NO: 17
 Db 1902 TGCAGGGCAAGTGTCAAGGCCCTCCCAGAAATGGATCAACGGGTCAGTGGCGA 1961
 Qy 26 -----IlearginleTyrasnThrArgAlaAlaLysCysileasnLysThrCy₈ 41
 Db 1962 GAACATCTCTCGTCAGATGTCAGACATTTCACAGATGTTCCACCGAGCGTGC 2021
 Qy 42 AsnC₈Tyr 44
 Db 2022 GGATGCCAT 2030

RESULT 15
 US-10-044-359-17
 ; Sequence 17, Application US/10044359
 ; Publication No. US20020160454A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herrman, Rafael
 ; APPLICANT: Wong, James F.
 ; APPLICANT: Lee, Jian-Ming
 ; TITLE OF INVENTION: SCORPION TOXINS
 ; FILE REFERENCE: BB1367 US NA
 ; CURRENT APPLICATION NUMBER: US/10/044,359
 ; CURRENT FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 09/599,416
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/140,227
 ; PRIOR FILING DATE: 1999-06-22
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97